

SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> Coccidian parasite casein kinase I as a
chemotherapeutic target for antiprotozoal agents

<130> 21554 PCT

<150> 60/537,094

<151> 2004-01-16

<160> 45

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2182

<212> DNA

<213> Eimeria tenella

<220>

<221> CDS

<222> (715)...(1722)

<400> 1

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tccctgagggc agcgtgcatg tatggtccgg cagccagctt ggtgtcgag ccgtacttct 180
tggaagcgag agagactgtg ggagagcgca aatcactcca gccgcttcca ggggagtctg 240
gggaccgcag gacgcttgga ggctgcctgc cggcataaac aggaacaagc gcattcttat 300
tcttctgtgg ttgctgagtt ctggctgcgt tcaagggggt tcacctcttc cccttctggc 360
gagtttttgc tgcgtcttcc cctaagaagc agcgccacgt gcgtggcggt cctcagcctg 420
acgcggtgca ccttttacgt aagagcgtcg atagcatcgg tcacttacag cagcgtgctg 480
ctgcttccgt gacctttaca ctgcttggtg cgggccgtct tgtagagggg ccatctgctt 540
gttcgctgct ggacgcagac ccggcgcccc acatttccgg cagccgggca gttgagataa 600
accggetgcc cgggtggcgt cgaaattgaa gcaggatctc tacagtaagg aacaaatcgc 660
gctattttta aggagtgtgt atacttgggg cgttactcgt gagtattgct gatg atg 717
                                     Met
                                     1

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gac gtc cgt gtg ggg ggt aag tat cgt ttg ggg agg aag att ggg agc 765
Asp Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser
      5              10              15

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gga tcc ttc ggc gac atc tac ctt ggt acg aac atc tca aca gga gat 813
Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asn Ile Ser Thr Gly Asp
      20              25              30

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gaa gtc gct atc aaa ttg gaa agc gtg cgg tct agg cat cca caa cta 861
Glu Val Ala Ile Lys Leu Gly Ser Val Arg Ser Arg His Pro Gln Leu
      35              40              45

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atc tat gaa agc aag ctg tac aaa atc cta acg ggt gga atc gga atc	909
Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly Ile	
50 55 60 65	
ccg act ctt tac tgg tat ggg atc gag ggg gat tac aac gtt atg att	957
Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Ile	
70 75 80	
att gag ctt ttg ggc ccg tct ctt gag gac ctc ttc agc att tgc aac	1005
Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn	
85 90 95	
aga aag ctt tct ttg aag act gtt ctg atg ctc gcc gac caa atg cta	1053
Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu	
100 105 110	
aat cgt att gag ttc gtc cac agc aga cat ttc atc cat cga gac atc	1101
Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp Ile	
115 120 125	
aag cct gac aat ttt ttg atc ggt agg ggc aaa aag atg tcc att gtt	1149
Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile Val	
130 135 140 145	
ttt gct atc gac ttt ggc ctc gca aag aag tac aga gat ccc aga aca	1197
Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg Thr	
150 155 160	
cag tcc cat att cct tat cga gaa ggg aag aac ctg aca ggt acc gcg	1245
Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala	
165 170 175	
agg tac gcc tct gtg aac acc cac ttg gga ata gaa cag agc agg cgc	1293
Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg	
180 185 190	
gat gat ctg gaa gcg ctc ggc tac gtc tta atg tac ttc aac aga ggt	1341
Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly	
195 200 205	
tcc tta ccc tgg caa gga tta aag gcc act acg aag aaa gat aaa tat	1389
Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr	
210 215 220 225	
gac aag att atg gag aag aag atg tcc acc cct att gaa gtc ctt tgc	1437
Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu Cys	
230 235 240	
aaa caa ttt cca ttt gag ttt atc aca tat ctg aac tat tgc cgg tct	1485
Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser	
245 250 255	
ctg cga ttc gaa gat cgc ccg gac tat tcc tat ttg aga cgg ttg ttc	1533
Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu Phe	
260 265 270	

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aag gat ctt ttc ttc cgt gag gga tac cag tat gac ttt ata ttc gat 1581
Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp
275 280 285

tgg aca ttt ctg cat gct gag aga gag cgc gag cgt caa aga cga tcg 1629
Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg Ser
290 295 300 305

atg gtc aac caa ggc gca gaa tca ggg aac cag tgg aga cga gac gcg 1677
Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp Ala
310 315 320

tcg ggc aga gat cca ctt gga cgg ttg cct cag tta gaa ccg taa 1722
Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro *
325 330 335

tctctttacg ggcagattgc cgtacgggtc ttctgctcat tcagtggcag tgccaccgca 1782
gtgctatctg aggctgtggc ttcaggatgt ggtagccagt taccatgggc acttgccctc 1842
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<210> 2

<211> 335

<212> PRT

<213> Eimeria tenella

<400> 2

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20 25 30
Asp Glu Val Ala Ile Lys Leu Glu Ser Val Arg Ser Arg His Pro Gln
35 40 45
Leu Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly
50 55 60
Ile Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met
65 70 75 80
Ile Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys
85 90 95
Asn Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met
100 105 110
Leu Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp
115 120 125
Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile
130 135 140
Val Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg
145 150 155 160
Thr Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr
165 170 175

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Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg
 180 185 190
 Arg Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg
 195 200 205
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys
 210 215 220
 Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
 225 230 235 240
 Cys Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg
 245 250 255
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu
 260 265 270
 Phe Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe
 275 280 285
 Asp Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg
 290 295 300
 Ser Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp
 305 310 315 320
 Ala Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro
 325 330 335

<210> 3

<211> 2076

<212> DNA

<213> *Toxoplasma gondii*

<220>

<221> CDS

<222> (898)...(1872)

<400> 3

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 ccctttctat gcgttgccac ccgtctgcaa gtatcgcgtc tttcgtctca tcagtgtttt 180
 tctttgcgtg tcgcgttcgg gacgcccttt tctctcctca actaactagc agacgtttct 240
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 tgcaacttgt cgcctgtcgt tcttcacttc ttctctccca tctctcgtg actcttcttc 360
 tcgagaactc tttctgtcga actctcaacc cccacgactg ctgggtttcgt ggccgtcccg 420
 catgcacctt gtgtcccgc gccttggcgc aaacacccgc tttctctgct gtccgccttc 480
 cgggtggactt ctctccgtgt tttttcgtgt tgccaaaagt ttgtctgctt tgacgtttct 540
 ctgctcaccc attgcccgt cttgatgagg aacgctccac attgacagcg aactcacagc 600
 acgcaccctc cgcgagcgga ctttcacgag cgaggcaaga atccatcgtc accccgccta 660
 cacgtacact actccacttg ggtgcccacg cgcggttct gggagacaga gacggctctc 720
 gttttccgtg tcagaacttt gtcgagggaaa cgctgctgct ggcagcgggg attgtgacct 780
 ccctcggcga acggggcgaag ccgcccgtgc gcgcgtcgcg actcagctga ggcgacaggc 840
 ggtcggcggc gtgacctctc tttctttttg cattcggccc tgattgcagc acgaagg atg 900
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gag gtc agg gtc gga ggc aag tac cga ctt ggt cgg aag atc ggc agc 948
 Glu Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser
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ggg tca ttc ggt gat att tat atc ggt gca aac att ttg acg ggg gat	996
Gly Ser Phe Gly Asp Ile Tyr Ile Gly Ala Asn Ile Leu Thr Gly Asp	
20 25 30	
gag gtg gcg atc aag ttg gag tct atc aag tcg aag cac ccg cag ctg	1044
Glu Val Ala Ile Lys Leu Glu Ser Ile Lys Ser Lys His Pro Gln Leu	
35 40 45	
ctc tat gag tcg aag ctg tac aaa ctg ctg gct ggc ggc att ggg att	1092
Leu Tyr Glu Ser Lys Leu Tyr Lys Leu Leu Ala Gly Gly Ile Gly Ile	
50 55 60 65	
ccc atg gtc cac tgg tac ggc atc gaa gga gac tac aat gtt atg gtt	1140
Pro Met Val His Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Val	
70 75 80	
atc gac ctt ctc ggc cct tct ctg gag gac ctt ttc agt atc tgc aat	1188
Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn	
85 90 95	
cgc aaa ctc tct ctc aag acg gtg ttg atg ctc gca gac cag atg ctc	1236
Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu	
100 105 110	
aac cgc atc gag ttt gtc cat agc aag aac ttc atc cat cgc gat atc	1284
Asn Arg Ile Glu Phe Val His Ser Lys Asn Phe Ile His Arg Asp Ile	
115 120 125	
aaa ccc gac aac ttc ctc att ggc cgt gga aag aag atg tcc gtc gtc	1332
Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Val Val	
130 135 140 145	
tac atc atc gat ttc ggt ttg gca aag aaa tat cga gac cca aag act	1380
Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Lys Thr	
150 155 160	
cag caa cat atc cca tac agg gaa ggc aag aac cta aca ggc aca gcg	1428
Gln Gln His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala	
165 170 175	
cgt tac gct tcc atc aac acc cac ctg ggg atc gag cag agt cgg cga	1476
Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg	
180 185 190	
gac gac cta gag gcg ctc ggt tac gtt ctc atg tac ttc aat aga ggt	1524
Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly	
195 200 205	
tct ctt ccg tkg cag ggt ctg aag gcg acg acg aag aag gac aaa tac	1572
Ser Leu Pro Xaa Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr	
210 215 220 225	
gac aag att atg gag aag aaa atg tct act ccc atc gaa att ttg tgc	1620
Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu Cys	
230 235 240	

aag cat ttc cca ttc gag ttc atc acc tac ttg aat tac tgc cgg tcc 1668
Lys His Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser
245 250 255

ctg cgc ttc gag gat cgt cct gac tac gca tac ttg cga cgc ctg ttc 1716
Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Arg Arg Leu Phe
260 265 270

aaa gac ttg ttt ttt aga gag gga tat cag tac gac ttc atc ttc gac 1764
Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp
275 280 285

tgg act ttc atc aac acg gag aag gat cgc gcg agt cga aga agc cag 1812
Trp Thr Phe Ile Asn Thr Glu Lys Asp Arg Ala Ser Arg Arg Ser Gln
290 295 300 305

caa gtt tat gtg gaa gac aac cgg caa gtt gag gag aat cag aac gag 1860
Gln Val Tyr Val Glu Asp Asn Arg Gln Val Glu Glu Asn Gln Asn Glu
310 315 320

ttg ccg atg tag ggtggtcggg gtgcggaggc cggcggggag cgtggagtc 1912
Leu Pro Met *

gctgagtcctg gaagtctgca gactgtgctc tggcactcga cccacttggt tgtgtttccc 1972
tcgactcgcg caggtcgagg aaaacagaga cgaacagggt acccaggagt gtttttggtc 2032
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<210> 4

<211> 324

<212> PRT

<213> Toxoplasma gondii

<400> 4

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20 25 30
Asp Glu Val Ala Ile Lys Leu Glu Ser Ile Lys Ser Lys His Pro Gln
35 40 45
Leu Leu Tyr Glu Ser Lys Leu Tyr Lys Leu Leu Ala Gly Gly Ile Gly
50 55 60
Ile Pro Met Val His Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met
65 70 75 80
Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys
85 90 95
Asn Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met
100 105 110
Leu Asn Arg Ile Glu Phe Val His Ser Lys Asn Phe Ile His Arg Asp
115 120 125
Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Val
130 135 140
Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Lys
145 150 155 160

Thr Gln Gln His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr
 165 170 175
 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
 180 185 190
 Arg Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg
 195 200 205
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys
 210 215 220
 Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu
 225 230 235 240
 Cys Lys His Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg
 245 250 255
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Arg Arg Leu
 260 265 270
 Phe Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe
 275 280 285
 Asp Trp Thr Phe Ile Asn Thr Glu Lys Asp Arg Ala Ser Arg Arg Ser
 290 295 300
 Gln Gln Val Tyr Val Glu Asp Asn Arg Gln Val Glu Glu Asn Gln Asn
 305 310 315 320
 Glu Leu Pro Met

<210> 5
 <211> 2373
 <212> DNA
 <213> Toxoplasma gondii

<220>
 <221> CDS
 <222> (119)...(1417)

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 atg gcg cac cat caa gac acc cgc aac cac acg ggg gtc gga ccc tct 166
 Met Ala His His Gln Asp Thr Arg Asn His Thr Gly Val Gly Pro Ser
 1 5 10 15
 tcg tct atc cct ctg aaa gat ttg aag atc gcc ggc gtc tgg aaa atc 214
 Ser Ser Ile Pro Leu Lys Asp Leu Lys Ile Ala Gly Val Trp Lys Ile
 20 25 30
 ggc aga aaa atc gga tcc ggt tcc ttc ggc gac ata tac aaa ggc ctg 262
 Gly Arg Lys Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Lys Gly Leu
 35 40 45
 aat tct cag acc ggt cag gag gtg gcg ctg aag gtc gaa agc acc aag 310
 Asn Ser Gln Thr Gly Gln Glu Val Ala Leu Lys Val Glu Ser Thr Lys
 50 55 60
 gcg aag cat ccg cag ttg ctg tac gaa tac aaa ctt ttg aag cat ttg 358
 Ala Lys His Pro Gln Leu Leu Tyr Glu Tyr Lys Leu Leu Lys His Leu
 65 70 75 80

cag gga gga acg ggc att gct caa gtg ttc tgt tgc gag act gcg ggc 406
 Gln Gly Gly Thr Gly Ile Ala Gln Val Phe Cys Cys Glu Thr Ala Gly
 85 90 95

gac cat aac atc atg gcc atg gag ttg ctc gga cct tct tta gag gac 454
 Asp His Asn Ile Met Ala Met Glu Leu Leu Gly Pro Ser Leu Glu Asp
 100 105 110

gtc ttc aac ttg tgc aat cgc acc ttc tct ctc aaa acc att ctt ctt 502
 Val Phe Asn Leu Cys Asn Arg Thr Phe Ser Leu Lys Thr Ile Leu Leu
 115 120 125

ctc gcc gac cag ttt ctg caa cgc gtc gag tac atc cac tcc aag aat 550
 Leu Ala Asp Gln Phe Leu Gln Arg Val Glu Tyr Ile His Ser Lys Asn
 130 135 140

ttc att cac aga gat atc aaa cca gat aac ttt ctt ctc ggc ggt gcc 598
 Phe Ile His Arg Asp Ile Lys Pro Asp Asn Phe Leu Leu Gly Gly Ala
 145 150 155 160

ggc aat caa aac acg atc tac gtg atc gac ttc ggc ctg gcg aag aag 646
 Gly Asn Gln Asn Thr Ile Tyr Val Ile Asp Phe Gly Leu Ala Lys Lys
 165 170 175

ttt cgc gat ccg aaa acg cac caa cat att ccg tac aga gaa aac aag 694
 Phe Arg Asp Pro Lys Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys
 180 185 190

aat ctc acg gga acg gcg cgc tac gcg tcc atc agt gcg cat ctg ggt 742
 Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Ile Ser Ala His Leu Gly
 195 200 205

tcc gag cag agt cgc cga gat gac ctc gaa gca gtc ggc tac gtt ctc 790
 Ser Glu Gln Ser Arg Arg Asp Leu Glu Ala Val Gly Tyr Val Leu
 210 215 220

atg tac ttc tgt cga gga ggc acg ctg cct tgg cag ggc atc aaa gcg 838
 Met Tyr Phe Cys Arg Gly Gly Thr Leu Pro Trp Gln Gly Ile Lys Ala
 225 230 235 240

aat acc aaa cag gag aag tac cac aag atc atg gag aag aag atg tcg 886
 Asn Thr Lys Gln Glu Lys Tyr His Lys Ile Met Glu Lys Lys Met Ser
 245 250 255

acg ccc gtc gag gtg cta tgc aag gga tat cca agc gaa ttt gcc aca 934
 Thr Pro Val Glu Val Leu Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr
 260 265 270

tac ttg cac tac tgc cgc tcc ttg cga ttc gag gac cga ccg gac tac 982
 Tyr Leu His Tyr Cys Arg Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr
 275 280 285

gcc tac ctc aag cga ctc ttt cga gat ctc tac atc aaa gag ggc tac 1030
 Ala Tyr Leu Lys Arg Leu Phe Arg Asp Leu Tyr Ile Lys Glu Gly Tyr
 290 295 300


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gat gac agt gac cgc gaa ttc gac tgg aca gtg aaa ctt tcg tcg cgc 1078
Asp Asp Ser Asp Arg Glu Phe Asp Trp Thr Val Lys Leu Ser Ser Arg
305 310 315 320

agt ctc gga ccg cca agc agt cga gcg caa cat gtt tta ctg agt caa 1126
Ser Leu Gly Pro Ser Ser Arg Ala Gln His Val Leu Leu Ser Gln
325 330 335

gac acc cga acg cga ggg aag cgg gag aca gat cga cct gtc gct gcg 1174
Asp Thr Arg Thr Arg Gly Lys Arg Glu Thr Asp Arg Pro Val Ala Ala
340 345 350

cgg agt ggc gac cgc gaa cga gga atc cat ttc agc aac ggg aac gtg 1222
Arg Ser Gly Asp Arg Glu Arg Gly Ile His Phe Ser Asn Gly Asn Val
355 360 365

ggc aat cct tcg atg gca acg aac ccc ggc ggc ctg tca gtc atg gtg 1270
Gly Asn Pro Ser Met Ala Thr Asn Pro Gly Gly Leu Ser Val Met Val
370 375 380

cat gaa cgc acg agt ctg gtg gat cag gga gac cgt ggg tcg cgc gaa 1318
His Glu Arg Thr Ser Leu Val Asp Gln Gly Asp Arg Gly Ser Arg Glu
385 390 395 400

act tct acg cgg aaa gaa gac gcg aag gac ggc aga tgg cca gga ggc 1366
Thr Ser Thr Arg Lys Glu Asp Ala Lys Asp Gly Arg Trp Pro Gly Gly
405 410 415

aga ttt tct tgt ctt cca ctg tta tgt cgg cgc tct ccg acg aag gcc 1414
Arg Phe Ser Cys Leu Pro Leu Leu Cys Arg Arg Ser Pro Thr Lys Ala
420 425 430

tag atgaactgcg gaggcgctcc tgccccgcga gttggcatct ctctccttca 1467
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ttgtcgttgt tcccctgcaa ctgcagtgcca cccttgacat cctcgtctct ctcttccctgt 1527
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aaagctttct tttccgctgg catgctggaa gaaggcagg aggcgacgat cctgcgagtc 2247
agggcgctcc cttgtttcca gtgagttaac cgaattgttt attgatatgc gtttgcatgc 2307
atcgacaatg gatcctagac acgcccgttt aaaatcagag gtattcctaa aaaaaaaaaa 2367
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<210> 6

<211> 432

<212> PRT

<213> Toxoplasma gondii

<400> 6

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Met Ala His His Gln Asp Thr Arg Asn His Thr Gly Val Gly Pro Ser
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Gly Arg Lys Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Lys Gly Leu
      35          40          45
Asn Ser Gln Thr Gly Gln Glu Val Ala Leu Lys Val Glu Ser Thr Lys
      50          55          60
Ala Lys His Pro Gln Leu Leu Tyr Glu Tyr Lys Leu Leu Lys His Leu
      65          70          75          80
Gln Gly Gly Thr Gly Ile Ala Gln Val Phe Cys Cys Glu Thr Ala Gly
      85          90          95
Asp His Asn Ile Met Ala Met Glu Leu Leu Gly Pro Ser Leu Glu Asp
      100          105          110
Val Phe Asn Leu Cys Asn Arg Thr Phe Ser Leu Lys Thr Ile Leu Leu
      115          120          125
Leu Ala Asp Gln Phe Leu Gln Arg Val Glu Tyr Ile His Ser Lys Asn
      130          135          140
Phe Ile His Arg Asp Ile Lys Pro Asp Asn Phe Leu Leu Gly Gly Ala
      145          150          155          160
Gly Asn Gln Asn Thr Ile Tyr Val Ile Asp Phe Gly Leu Ala Lys Lys
      165          170          175
Phe Arg Asp Pro Lys Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys
      180          185          190
Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Ile Ser Ala His Leu Gly
      195          200          205
Ser Glu Gln Ser Arg Arg Asp Asp Leu Glu Ala Val Gly Tyr Val Leu
      210          215          220
Met Tyr Phe Cys Arg Gly Gly Thr Leu Pro Trp Gln Gly Ile Lys Ala
      225          230          235          240
Asn Thr Lys Gln Glu Lys Tyr His Lys Ile Met Glu Lys Lys Met Ser
      245          250          255
Thr Pro Val Glu Val Leu Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr
      260          265          270
Tyr Leu His Tyr Cys Arg Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr
      275          280          285
Ala Tyr Leu Lys Arg Leu Phe Arg Asp Leu Tyr Ile Lys Glu Gly Tyr
      290          295          300
Asp Asp Ser Asp Arg Glu Phe Asp Trp Thr Val Lys Leu Ser Ser Arg
      305          310          315          320
Ser Leu Gly Pro Pro Ser Ser Arg Ala Gln His Val Leu Leu Ser Gln
      325          330          335
Asp Thr Arg Thr Arg Gly Lys Arg Glu Thr Asp Arg Pro Val Ala Ala
      340          345          350
Arg Ser Gly Asp Arg Glu Arg Gly Ile His Phe Ser Asn Gly Asn Val
      355          360          365
Gly Asn Pro Ser Met Ala Thr Asn Pro Gly Gly Leu Ser Val Met Val
      370          375          380

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His Glu Arg Thr Ser Leu Val Asp Gln Gly Asp Arg Gly Ser Arg Glu
 385 390 395 400
 Thr Ser Thr Arg Lys Glu Asp Ala Lys Asp Gly Arg Trp Pro Gly Gly
 405 410 415
 Arg Phe Ser Cys Leu Pro Leu Leu Cys Arg Arg Ser Pro Thr Lys Ala
 420 425 430

<210> 7
 <211> 543
 <212> DNA
 <213> Toxoplasma gondii (EST)

<400> 7
 agaatttcat tcacagagat atcaaaccag ataactttct tctcggcggt gccggcaatc 60
 aaaacacgat ctacgtgacg gacttcggcc tggcggaagaa gtttcgcat ccgaaaacgc 120
 accaacatat tccgtacaga gaaaacaaga atctcacggg aacggcgcg c tacgcgtcca 180
 tcagtgcgca tctgtgttcc gagcagagtc gccgagatga cctcgaagca gtcggctacg 240
 ttctcatgta cttctgtcga ggaggcacgc tgccttggca gggcatcaaa gcgaatacca 300
 aacaggagaa gtaccacaag atcatggaga agaagatgtc gacgcccgtc gaggtgctat 360
 gcaagggata tccaagcgaa tttgccacat acttgcaacta ctgccgctcc ttgcgattcg 420
 aggaccgacc ggactacgcc tacctcaagc gactctttcg agatctctac atcaaagagg 480
 gctacgatga cagtgaccgc gaattcgact ggacagtga a actttcgtcg cgcagtctcg 540
 gac 543

<210> 8
 <211> 341
 <212> DNA
 <213> Toxoplasma gondii (EST)

<400> 8
 gatatccaag cgaatttgcc acatacttgc actactgccg ctccttgcga ttcgaggacc 60
 gaccggacta cgcctacctc aagcgactct ttcgagatct ctacatcaaa gagggctacg 120
 atgacagtga ccgcgaattc gactggacag tgaaactttc gtcgcgcagt ctcggaccgc 180
 caagcagtcg agcgcaacat gttttactga gtcaagacac ccgaacgcga gggaagcggg 240
 agacagatcg acctgtcgtc gtgcggagtgc gcgaccgcga acgaggaatc catttcagca 300
 acgggaacgt gggcaatccc tccgatggca acgaaccccc g 341

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 9
 gatatcaaac cagataactt tcttctcggc 30

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 10
caaggagcgg cagtagtgca agt

23

<210> 11
<211> 21
<212> PRT
<213> Eimeria tenella (peptide)

<400> 11
Ala Lys Asp Leu Ile Arg Lys Met Leu Ala Tyr Val Pro Ser Met Arg
1 5 10 15
Ile Ser Ala Arg Asp
20

<210> 12
<211> 20
<212> PRT
<213> Eimeria tenella (peptide)

<400> 12
Ala Val Lys Val Ile Ser Lys Arg Gln Val Lys Gln Lys Thr Asp Lys
1 5 10 15
Glu Leu Leu Leu
20

<210> 13
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 13
Arg Arg Lys Asp Leu His Asp Asp Glu Glu Asp Glu Ala Met Ser Ile
1 5 10 15
Thr Ala

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 14
Arg Arg Ala Asp Asp Ser Asp Asp Asp Asp Asp
1 5 10

<210> 15
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 15

Pro Leu Ala Arg Thr Leu Ser Val Ala Gly Leu Pro Gly Lys Lys
1 5 10 15

<210> 16

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 16

Met His Lys Asn Glu Thr Val Glu Cys Leu Lys
1 5 10

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 17

Asp Asp Asp Glu Glu Ser Ile Thr Arg Arg
1 5 10

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 18

Leu Arg Arg Ala Ser Leu Gly
1 5

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 19

Lys Arg Arg Arg Ala Leu Ser Val Ala Ser Leu Pro Gly Leu
 1 5 10

<210> 20
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 20
 Arg Arg Arg Glu Glu Glu Thr Glu Glu Glu
 1 5 10

<210> 21
 <211> 324
 <212> PRT
 <213> Plasmodium falciparum

<400> 21
 Met Glu Ile Arg Val Ala Asn Lys Tyr Ala Leu Gly Lys Lys Leu Gly
 1 5 10 15
 Ser Gly Ser Phe Gly Asp Ile Tyr Val Ala Lys Asp Ile Val Thr Met
 20 25 30
 Glu Glu Phe Ala Val Lys Leu Glu Ser Thr Arg Ser Lys His Pro Gln
 35 40 45
 Leu Leu Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Gly Gly Ile Gly
 50 55 60
 Val Pro Lys Val Tyr Trp Tyr Gly Ile Glu Gly Asp Phe Thr Ile Met
 65 70 75 80
 Val Leu Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Thr Leu Cys
 85 90 95
 Asn Arg Lys Phe Ser Leu Lys Thr Val Arg Met Thr Ala Asp Gln Met
 100 105 110
 Leu Asn Arg Ile Glu Tyr Val His Ser Lys Asn Phe Ile His Arg Asp
 115 120 125
 Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Val Thr Leu
 130 135 140
 Ile His Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ser Arg
 145 150 155 160
 Ser His Thr Ser Tyr Pro Tyr Lys Glu Gly Lys Asn Leu Thr Gly Thr
 165 170 175
 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
 180 185 190
 Arg Asp Asp Ile Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Leu Arg
 195 200 205
 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ile Ser Lys Lys Asp Lys
 210 215 220
 Tyr Asp Lys Ile Met Glu Lys Lys Ile Ser Thr Ser Val Glu Val Leu
 225 230 235 240
 Cys Arg Asn Ala Ser Phe Glu Phe Val Thr Tyr Leu Asn Tyr Cys Arg
 245 250 255
 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Thr Tyr Leu Arg Arg Leu
 260 265 270

Leu Lys Asp Leu Phe Ile Arg Glu Gly Phe Thr Tyr Asp Phe Leu Phe
 275 280 285
 Asp Trp Thr Cys Val Tyr Ala Ser Glu Lys Asp Lys Lys Lys Met Leu
 290 295 300
 Glu Asn Lys Asn Arg Phe Asp Gln Thr Ala Asp Gln Glu Gly Arg Asp
 305 310 315 320
 Gln Arg Asn Asn

<210> 22
 <211> 353
 <212> PRT
 <213> Leshmania major

<400> 22
 Met Asn Val Glu Leu Arg Val Gly Asn Arg Tyr Arg Ile Gly Gln Lys
 1 5 10 15
 Ile Gly Ser Gly Ser Phe Gly Glu Ile Phe Arg Gly Thr Asn Ile Gln
 20 25 30
 Thr Gly Asp Pro Val Ala Ile Lys Leu Glu Gln Val Lys Thr Arg His
 35 40 45
 Pro Gln Leu Thr Tyr Glu Ser Arg Phe Tyr Arg Ile Leu Gly Ser Gly
 50 55 60
 Gly Gly Ala Val Gly Ile Pro Met Met Phe Tyr His Gly Val Glu Gly
 65 70 75 80
 Glu Phe Asn Val Met Val Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp
 85 90 95
 Leu Phe Ser Phe Cys Gly Arg Arg Leu Ser Leu Lys Thr Thr Leu Met
 100 105 110
 Leu Ala Asp Gln Met Ile Ser Arg Ile Glu Phe Val His Ser Lys Ser
 115 120 125
 Val Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met Gly Thr Gly
 130 135 140
 Lys Lys Gly His His Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys
 145 150 155 160
 Tyr Arg Asp Pro Arg Thr His Ala His Ile Pro Tyr Lys Glu Gly Lys
 165 170 175
 Ser Leu Thr Gly Thr Ala Arg Tyr Cys Ser Ile Asn Thr His Met Gly
 180 185 190
 Val Glu Gln Gly Arg Arg Asp Asp Met Glu Gly Ile Gly Tyr Ile Leu
 195 200 205
 Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala His
 210 215 220
 Thr Lys Gln Glu Lys Tyr Asn Arg Ile Ser Glu Arg Lys Gln Thr Thr
 225 230 235 240
 Pro Val Glu Leu Leu Cys Lys Gly Phe Pro Ser Glu Phe Ala Ala Tyr
 245 250 255
 Met Asn Tyr Val Arg Ala Leu Arg Phe Glu Asp Lys Pro Asp Tyr Ser
 260 265 270
 Tyr Leu Lys Arg Met Phe Arg Asp Leu Phe Val Arg Glu Gly Tyr His
 275 280 285
 Val Asp Tyr Val Phe Asp Trp Thr Leu Lys Arg Ile His Glu Ser Leu
 290 295 300
 Gln Glu Gln Gln Ser Phe Pro Gly Gly Ser Asn Gly Gly Gly Ala Ala
 305 310 315 320

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<210> 23
<211> 330
<212> PRT
<213> Trypanosoma cruzi
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<210> 24
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 24
atggactaca aagacgatga cgacaaggag gtcagggtcg gaggcaagta cgcac 55

<210> 25
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 25
cggctctagat cagagggaga cgcgcgtcct gacc 34

<210> 26
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 26
atggactaca aagacgatga cgacaaggcg caccatcaag acaccgcaa c 51

<210> 27
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 27
cggctctagat caaaaaaaga acttacgccc acggcgt 37

<210> 28
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 28

ggcggatccg aaaatggact acaaagacga tgacgacaag gaggtcaggg tcggaggcaa 60
gtaccgac 68

<210> 29
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 29
ggcgtgatca aaaatggact acaaagacga tgacgacaag gcgcaccatc aagacacccg 60
caac 64

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 30
ggcctcgagg gccttcgtcg gagagcgccg acataacagt g 41

<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 31
ggcgtcgacg atgttatggt cgcccgagc ctcgcaaca 39

<210> 32
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 32
ggcgtcgacg atcttgtggt acttctctctg ttgtgtattc gctttgatgc 50

<210> 33
<211> 41
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 33

ggcctcgagc acgttcccgt tgctgaaatg gattcctcgt t

41

<210> 34

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 34

atggactaca aagacgatga cgacaaggac gtccgtgtgg ggggtaagta tcgtttg

57

<210> 35

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 35

cggctctagat cacggttcta actgaggcaa ccgtccaagt

40

<210> 36

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 36

ggcagatctg aaaatggact acaaagacga tgacgacaag gacgtccgtg tggggggtaa
gtatcgtttg

60

70

<210> 37

<211> 11

<212> PRT

<213> Eimeria tenella (peptide)

<400> 37

Ser Arg His Pro Gln Leu Ile Tyr Glu Ser Lys
1 5 10

<210> 38

<211> 12

<212> PRT

<213> Eimeria tenella (peptide)

<400> 38

Thr Val Leu Met Leu Ala Asp Gln Met Leu Asn Arg
1 5 10

<210> 39
<211> 11
<212> PRT
<213> Eimeria tenella (peptide)

<400> 39
Asp Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg
1 5 10

<210> 40
<211> 8
<212> PRT
<213> Eimeria tenella (peptide)

<400> 40
Thr Gln Ser His Ile Pro Tyr Arg
1 5

<210> 41
<211> 14
<212> PRT
<213> Eimeria tenella (peptide)

<400> 41
Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg
1 5 10

<210> 42
<211> 11
<212> PRT
<213> Eimeria tenella (peptide)

<400> 42
Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg
1 5 10

<210> 43
<211> 5
<212> PRT
<213> Eimeria tenella (peptide)

<400> 43
Asp Leu Phe Phe Arg
1 5

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 44
aaaatggggc agcaggaaag cactcttggg

30

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 45
gtttccgcag agcttcaaga gcatctgtt

29